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JUN 06 2002

TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/09/786,389A

TIME: 07:53:58

Input Set : N:\Crf3\06032002\I786389.raw

Output Set: N:\CRF3\06032002\I786389A.raw

1 <110> APPLICANT: Japan Science and Technology Corporation
 2 <120> TITLE OF INVENTION: Amino Acid Transporter And Gene Thereof
 3 <130> FILE REFERENCE: PC901338
 4 <140> CURRENT APPLICATION NUMBER: US/09/786,389A
 5 <141> CURRENT FILING DATE: 2001-09-03
 6 <160> NUMBER OF SEQ ID NOS: 27
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 9 <211> LENGTH: 4539
 10 <212> TYPE: DNA
 11 <213> ORGANISM: Homo sapiens
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 19 <221> NAME/KEY: 3'UTR
 20 <222> LOCATION: (1590)..(4474)
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 23 agagc atg gcg ggt gcg ggc ccg aag cgg cgc gcg cta gcg gcg ccg gcg 110
 24 Met Ala Gly Ala Gly Pro Lys Arg Arg Ala Leu Ala Ala Pro Ala
 25 1 5 10 15
 26 gcc gag gag aag gaa gag gcg cgg gag aag atg ctg gcc gcc aag agc 158
 27 Ala Glu Glu Lys Glu Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser
 28 20 25 30
 29 gcg gac ggc tcg gcg ccg gca ggc gag ggc gag ggc gtg acc ctg cag 206
 30 Ala Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln
 31 35 40 45
 32 cgg aac atc acg ctg ctc aac ggc gtg gcc atc atc gtg ggg acc att 254
 33 Arg Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile
 34 50 55 60
 35 atc ggc tcg ggc atc ttc gtg acg ccc acg ggc gtg ctc aag gag gca 302
 36 Ile Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala
 37 65 70 75
 38 ggc tcg ccg ggg ctg gcg ctg gtg gtg tgg gcc gcg tgc ggc gtc ttc 350
 39 Gly Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe
 40 80 85 90 95
 41 tcc atc gtg ggc gcg ctc tgc tac gcg gag ctc ggc acc acc atc tcc 398
 42 Ser Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser
 43 100 105 110
 44 aaa tcg ggc ggc gac tac gcc tac atg ctg gag gtc tac ggc tcg ctg 446

ENTERED

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45	Lys Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu	
46		115 120 125
47	ccc gcc ttc ctc aag ctc tgg atc gag ctg ctc atc atc cgg cct tca	494
48	Pro Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser	
49		130 135 140
50	tcg cag tac atc gtg gcc ctg gtc ttc gcc acc tac ctg ctc aag ccg	542
51	Ser Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro	
52		145 150 155
53	ctc ttc ccc acc tgc ccg gtg ccc gag gag gca gcc aag ctc gtg gcc	590
54	Leu Phe Pro Thr Cys Pro Val Pro Glu Glu Ala Ala Lys Leu Val Ala	
55		160 165 170 175
56	tgc ctc tgc gtg ctg ctg ctc acg gcc gtg aac tgc tac agc gtg aag	638
57	Cys Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys	
58		180 185 190
59	gcc gcc acc cgg gtc cag gat gcc ttt gcc gcc gcc aag ctc ctg gcc	686
60	Ala Ala Thr Arg Val Gln Asp Ala Phe Ala Ala Ala Lys Leu Leu Ala	
61		195 200 205
62	ctg gcc ctg atc atc ctg ctg ggc ttc gtc cag atc ggg aag ggt gat	734
63	Leu Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Asp	
64		210 215 220
65	gtg tcc aat cta gat ccc aac ttc tca ttt gaa ggc acc aaa ctg gat	782
66	Val Ser Asn Leu Asp Pro Asn Phe Ser Phe Glu Gly Thr Lys Leu Asp	
67		225 230 235
68	gtg ggg aac att gtg ctg gca tta tac agc ggc ctc ttt gcc tat gga	830
69	Val Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu Phe Ala Tyr Gly	
70		240 245 250 255
71	gga tgg aat tac ttg aat ttc gtc aca gag gaa atg atc aac ccc tac	878
72	Gly Trp Asn Tyr Leu Asn Phe Val Thr Glu Met Ile Asn Pro Tyr	
73		260 265 270
74	aga aac ctg ccc ctg gcc atc atc atc tcc ctg ccc atc gtg acg ctg	926
75	Arg Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu	
76		275 280 285
77	gtg tac gtg ctg acc aac ctg gcc tac ttc acc acc ctg tcc acc gag	974
78	Val Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr Leu Ser Thr Glu	
79		290 295 300
80	cag atg ctg tcg tcc gag gcc gtg gcc gtg gac ttc ggg aac tat cac	1022
81	Gln Met Leu Ser Ser Glu Ala Val Ala Val Asp Phe Gly Asn Tyr His	
82		305 310 315
83	ctg ggc gtc atg tcc tgg atc atc ccc gtc ttc gtg ggc ctg tcc tgc	1070
84	Leu Gly Val Met Ser Trp Ile Ile Pro Val Phe Val Gly Leu Ser Cys	
85		320 325 330 335
86	ttc ggc tcc gtc aat ggg tcc ctg ttc aca tcc tcc agg ctc ttc ttc	1118
87	Phe Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser Arg Leu Phe Phe	
88		340 345 350
89	gtg ggg tcc cgg gaa ggc cac ctg ccc tcc atc ctc tcc atg atc cac	1166
90	Val Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu Ser Met Ile His	
91		355 360 365
92	cca cag ctc ctc acc ccc gtg ccg tcc ctc gtg ttc acg tgt gtg atg	1214
93	Pro Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe Thr Cys Val Met	

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94          370          375          380
95  acg ctg ctc tac gcc ttc tcc aag gac atc ttc tcc gtc atc aac ttc 1262
96  Thr Leu Leu Tyr Ala Phe Ser Lys Asp Ile Phe Ser Val Ile Asn Phe
97          385          390          395
98  ttc agc ttc ttc aac tgg ctc tgc gtg gcc ctg gcc atc atc ggc atg 1310
99  Phe Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met
100  400          405          410          415
101  atc tgg ctg cgc cac aga aag cct gag ctt gag cgg ccc atc aag gtg 1358
102  Ile Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val
103          420          425          430
104  aac ctg gcc ctg cct gtg ttc ttc atc ctg gcc tgc ctc ttc ctg atc 1406
105  Asn Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile
106          435          440          445
107  gcc gtc tcc ttc tgg aag aca ccc gtg gag tgt ggc atc ggc ttc acc 1454
108  Ala Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr
109          450          455          460
110  atc atc ctc agc ggg ctg ccc gtc tac ttc ttc ggg gtc tgg tgg aaa 1502
111  Ile Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys
112          465          470          475
113  aac aag ccc aag tgg ctc ctc cag ggc atc ttc tcc acg acc gtc ctg 1550
114  Asn Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu
115  480          485          490          495
116  tgt cag aag ctc atg cag gtg gtc ccc cag gag aca tag ccaggaggcc 1599
117  Cys Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr
118          500          505
119  gagtggctgc cggaggagca tgcgcagagg ccagttaaag tagatcacct cctcgaaccc 1659
120  actccgggttc cccgcaaccc acagctcagc tgcccatccc agtccctcgc cgtccctccc 1719
121  aggtcgggca gtggaggctg ctgtgaaaac tctggtacga atctcatccc tcaactgagg 1779
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125  ttctcctgcc ccaagggccc agaccctggg caaacagagc tactgagact tggaaacctca 2019
126  ttgtacgac agacttgac tgaagccgga cagctgcccga gacacatggg cttgtgacat 2079
127  tcgtgaaaac caaccctgtg ggcttatgtc tctgccttag ggtttgaga gtggaaactc 2139
128  agccgtaggg tggcactggg agggggtggg ggatctgggc aagggtgggtg attcctccca 2199
129  ggaggtgctt gaggccccga tggactcctg accataatcc tagccccgag acaccatcct 2259
130  gagccaggga acagccccag ggttgggggg tgccggcatc tcccctagct caccaggcct 2319
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138  tgcagagagg gaactagggc accccttgtt tctgttttcc cagtgaattt ttttcgctat 2799
139  gggaggcagc cgaggcctgg ccaatgcggc ccactttcct gagctgtcgc tgccctcatg 2859
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142  ggtccagcgt cactccagtg ctcagctgtg gctggaggag ctggcctgtg gcacagccct 3039

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143 gagtgtccca agccgggagc caacgaagcc ggacacggct tcaactgacca gcggtgtctc 3099
144 aagccgcaag ctctcagcaa gtgcccagtg gagcctgccg cccccacctg ggcaccggga 3159
145 cccctcacc atccagtggg cccggagaaa cctgatgaac agtttgggga ctcaggacca 3219
146 gatgtccgtc tctcttgctt gaggaatgaa gacctttatt caccctgcc ccgttgcttc 3279
147 ccgtgcaca tggacagact tcacagcgct tgctcatagg acctgcatcc ttcttgggga 3339
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149 ggtggactga ctgtgttggg caagacctct tccctctggg cctgttctct tggctgcaaa 3459
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165 gccatccact gtgacgtcgg ccgaccaggc tggacaccct ctgccgagta atgacgtgtg 4419
166 tggctgggac cttctttatt ctgtgttaat ggctaacctg ttacactggg ctgggttggg 4479
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169 <210> SEQ ID NO: 2

170 <211> LENGTH: 507

171 <212> TYPE: PRT

172 <213> ORGANISM: Homo sapiens

173 <400> SEQUENCE: 2

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178 Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln Arg
179      35             40             45
180 Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile Ile
181      50             55             60
182 Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala Gly
183      65             70             75             80
184 Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe Ser
185      85             90             95
186 Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser Lys
187      100            105            110
188 Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu Pro
189      115            120            125
190 Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser Ser
191      130            135            140
192 Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro Leu

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193      145      150      155      160
194 Phe Pro Thr Cys Pro Val Pro Glu Glu Ala Ala Lys Leu Val Ala Cys
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196 Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys Ala
197      180      185      190
198 Ala Thr Arg Val Gln Asp Ala Phe Ala Ala Ala Lys Leu Leu Ala Leu
199      195      200      205
200 Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Asp Val
201      210      215      220
202 Ser Asn Leu Asp Pro Asn Phe Ser Phe Glu Gly Thr Lys Leu Asp Val
203      225      230      235      240
204 Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu Phe Ala Tyr Gly Gly
205      245      250      255
206 Trp Asn Tyr Leu Asn Phe Val Thr Glu Glu Met Ile Asn Pro Tyr Arg
207      260      265      270
208 Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu Val
209      275      280      285
210 Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr Leu Ser Thr Glu Gln
211      290      295      300
212 Met Leu Ser Ser Glu Ala Val Ala Val Asp Phe Gly Asn Tyr His Leu
213      305      310      315      320
214 Gly Val Met Ser Trp Ile Ile Pro Val Phe Val Gly Leu Ser Cys Phe
215      325      330      335
216 Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser Arg Leu Phe Phe Val
217      340      345      350
218 Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu Ser Met Ile His Pro
219      355      360      365
220 Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe Thr Cys Val Met Thr
221      370      375      380
222 Leu Leu Tyr Ala Phe Ser Lys Asp Ile Phe Ser Val Ile Asn Phe Phe
223      385      390      395      400
224 Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met Ile
225      405      410      415
226 Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val Asn
227      420      425      430
228 Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile Ala
229      435      440      445
230 Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr Ile
231      450      455      460
232 Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys Asn
233      465      470      475      480
234 Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu Cys
235      485      490      495
236 Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr
237      500      505
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 3455
241 <212> TYPE: DNA
242 <213> ORGANISM: Rat

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VERIFICATION SUMMARY

DATE: 06/03/2002

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TIME: 07:53:59

Input Set : N:\Crf3\06032002\I786389.raw

Output Set: N:\CRF3\06032002\I786389A.raw

L:570 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:1106 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
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L:1109 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:672
L:1112 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:720
L:1175 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:48
L:1202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:480
L:1205 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:528
L:1208 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:576
L:1211 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:624
L:1214 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:672
L:1217 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:720
L:1220 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:768
L:1226 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:864
L:1229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:912
L:1232 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:960
L:1235 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:1008
L:1238 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:1056
L:1244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:1152
L:1247 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:1200
L:1250 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:1248
L:1262 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:1440
L:1275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27